

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
 - (B) STREET: 1007 MARKET STREET
 - (C) CITY: WILMINGTON
 - (D) STATE: DELAWARE
 - (E) COUNTRY: USA
 - (F) ZIP: 19898
 - (G) TELEPHONE: 302-992-4926
 - (H) TELEFAX: 302-773-0164
 - (I) TELEX: 6717325
- (ii) TITLE OF INVENTION: PLANT AMINO ACID BIOSYNTHETIC ENZYMES
- (iii) NUMBER OF SEQUENCES: 43
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: DISKETTE, 3.50 INCH
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
 - (D) SOFTWARE: MICROSOFT WORD VERSION 7.0A
- (v) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/048,771
 - (B) FILING DATE: JUNE 6, 1997
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MAJARIAN, WILLIAM R.
 - (B) REGISTRATION NUMBER: 41,173
 - (C) REFERENCE/DOCKET NUMBER: BB-1087

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 908 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: csiln.pk0042.a3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ACGCGGGACA GATAAGTGGC ATGGACGAGC CGCTGGAGAT CCCTGTGCTG AACGACCTCA      60
CCATGGTTCT GGGCTCCATA GCGCAGTCGA GAGCAACCGG CGTGGTGGTC GACTTCAGCG      120
AGCCTTCAGC TGTTTACGAC AATGTCAAGC AGGCAGCGGC GTTGGTCTG AGCAGCGTCG      180
TCTACGTTCC GAAAATCGAG CTAGAGACAG TGACTGAACT GTCAGCGTTC TGCGAGAAGG      240
CAAGCGGCTG CTTGGTTGCG CCAACGCTGT CGATTGGGTC CGTGCTCCTT CAGCAAGCGG      300
CTATACAGGC CTCGTTCCAC TACAGCAACG TTGAGATTGT GGAATCGAGA CCAAACCCAT      360
CGGATCTTCC ATCGCAAGAT GCAATCCAGA TTGCAAACAA CATATCAGAC CTTGGTCAGA      420
TATACAACAG GGAAGATATG GATTCCAGCA GTCCAGCCAG AGGCCAGCTG CTCGGGGAAG      480
ACGGAGTGCG CGTGCACAGC ATGGTTCTCC CTGGTCTCGT CTCCAGCACG TCGATCAACT      540
TCTCTGGCCC AGGAGAGATG TACACCTTAC GGCATGACGT TGCGAATGTT CAGTGCCTGA      600
TGCCAGGACT GATCCTGGCG ATACGGAAGG TGGTGCGGTT CAAGAACTTG ATTTATGGGC      660
TAGAGAAGTT CTTGTAGTGA ACAACAAACA ACCAATGCAA AACATCGACA GGCAACAGGC      720
AAGGCAGATA TCATCTGACG TCGCAACAAC CAAAACGACA GAGATTGGA AAATAAAGGC      780
TGCACAGAAG ACGTCTGGGG TTTTGTGTGC ACCAGGCTGC GCAGAGAACG TCTGTCATTT      840
TGTGTGCACC ACTACGGCAC TACCTGCTGA GCGCGATTTT TATAAAAAAG GCATGGGAGG      900
GAGATCAT                                         908
  
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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: csiln.pk0042.a3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Ala Gly Gln Ile Ser Gly Met Asp Glu Pro Leu Glu Ile Pro Val Leu
1           5           10           15
  
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Asn Asp Leu Thr Met Val Leu Gly Ser Ile Ala Gln Ser Arg Ala Thr
 20 25 30
 Gly Val Val Val Asp Phe Ser Glu Pro Ser Ala Val Tyr Asp Asn Val
 35 40 45
 Lys Gln Ala Ala Ala Phe Gly Leu Ser Ser Val Val Tyr Val Pro Lys
 50 55 60
 Ile Glu Leu Glu Thr Val Thr Glu Leu Ser Ala Phe Cys Glu Lys Ala
 65 70 75 80
 Ser Gly Cys Leu Val Ala Pro Thr Leu Ser Ile Gly Ser Val Leu Leu
 85 90 95
 Gln Gln Ala Ala Ile Gln Ala Ser Phe His Tyr Ser Asn Val Glu Ile
 100 105 110
 Val Glu Ser Arg Pro Asn Pro Ser Asp Leu Pro Ser Gln Asp Ala Ile
 115 120 125
 Gln Ile Ala Asn Asn Ile Ser Asp Leu Gly Gln Ile Tyr Asn Arg Glu
 130 135 140
 Asp Met Asp Ser Ser Ser Pro Ala Arg Gly Gln Leu Leu Gly Glu Asp
 145 150 155 160
 Gly Val Arg Val His Ser Met Val Leu Pro Gly Leu Val Ser Ser Thr
 165 170 175
 Ser Ile Asn Phe Ser Gly Pro Gly Glu Met Tyr Thr Leu Arg His Asp
 180 185 190
 Val Ala Asn Val Gln Cys Leu Met Pro Gly Leu Ile Leu Ala Ile Arg
 195 200 205
 Lys Val Val Arg Phe Lys Asn Leu Ile Tyr Gly Leu Glu Lys Phe Leu
 210 215 220

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: rls2.pk0017.d3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGATTGGCA GGAGAAATGC AGCAAAGGTC CTCTGCTCAA CGCAGATGCC GCCATCTCAG	60
AGCACAATCA AGGTTGTTAT CATTGGGGCG ACAAAGAGA TTGGAAGAAC GGCAATAGCG	120
GCAGTAAGTA AAGCAAGGGG AATGGAGCTT GCAGGGGCCA TAGATTCTCA GTGTATAGGC	180
CTAGATGCAG GAGAGATAAG TGGCATGGGA AGAACCCTGG AAATCCGGT GCTCAATGAT	240
CTCACAATGG TTCTGGGCTC AATTGCACAA ACCAGAGCAA CTGGAGTGGT GGTGATTTT	300
AGTGAACCTT CAACTGTTTA TGATAATGTC AAACAGGCA	339

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: rls2.pk0017.d3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Lys Ile Gly Arg Arg Asn Ala Ala Lys Val Leu Cys Ser Thr Gln Met
1           5           10           15
Pro Pro Ser Gln Ser Thr Ile Lys Val Val Ile Ile Gly Ala Thr Lys
20           25           30
Glu Ile Gly Arg Thr Ala Ile Ala Ala Val Ser Lys Ala Arg Gly Met
35           40           45
Glu Leu Ala Gly Ala Ile Asp Ser Gln Cys Ile Gly Leu Asp Ala Gly
50           55           60
Glu Ile Ser Gly Met Gly Arg Thr Leu Glu Ile Pro Val Leu Asn Asp
65           70           75           80
Leu Thr Met Val Leu Gly Ser Ile Ala Gln Thr Arg Ala Thr Gly Val
85           90           95
Val Val Asp Phe Ser Glu Pro Ser Thr Val Tyr Asp Asn Val Lys Gln
100          105          110
Ala

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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Synechocystus sp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Met Ala Asn Gln Asp Leu Ile Pro Val Val Val Asn Gly Ala Ala Gly
1           5           10           15
Lys Met Gly Arg Glu Val Ile Lys Ala Val Ala Gln Ala Pro Asp Leu
20           25           30
Gln Leu Val Gly Ala Val Asp His Asn Pro Ser Leu Gln Gly Gln Asp
35           40           45
Ile Gly Glu Val Val Gly Ile Ala Pro Leu Glu Val Pro Val Leu Ala
50           55           60

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Asp Leu Gln Ser Val Leu Val Leu Ala Thr Gln Glu Lys Ile Gln Gly
 65 70 75 80
 Val Met Val Asp Phe Thr His Pro Ser Gly Val Tyr Asp Asn Val Arg
 85 90 95
 Ser Ala Ile Ala Tyr Gly Val Arg Pro Val Val Gly Thr Thr Gly Leu
 100 105 110
 Ser Glu Gln Gln Ile Gln Asp Leu Gly Asp Phe Ala Glu Lys Ala Ser
 115 120 125
 Thr Gly Cys Leu Ile Ala Pro Asn Phe Ala Ile Gly Val Leu Leu Met
 130 135 140
 Gln Gln Ala Ala Val Gln Ala Cys Gln Tyr Phe Asp His Val Glu Ile
 145 150 155 160
 Ile Glu Leu His His Asn Gln Lys Ala Asp Ala Pro Ser Gly Thr Ala
 165 170 175
 Ile Lys Thr Ala Gln Met Leu Ala Glu Met Gly Lys Thr Phe Asn Pro
 180 185 190
 Pro Ala Val Glu Glu Lys Glu Thr Ile Ala Gly Ala Lys Gly Gly Leu
 195 200 205
 Gly Pro Gly Gln Ile Pro Ile His Ser Ile Arg Leu Pro Gly Leu Ile
 210 215 220
 Ala His Gln Glu Val Leu Phe Gly Ser Pro Gly Gln Leu Tyr Thr Ile
 225 230 235 240
 Arg His Asp Thr Thr Asp Arg Ala Cys Tyr Met Pro Gly Val Leu Leu
 245 250 255
 Gly Ile Arg Lys Val Val Glu Leu Lys Gly Leu Val Tyr Gly Leu Glu
 260 265 270
 Lys Leu Leu
 275

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1012 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: chp2.pk0008.h4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TATTGCCAGA GATGTGTGGT AATGGAGTCC GTTGCTTCGC TCGGTTTATA GCCGAGATTG	60
AAAATCTGCA GGGGACAAAT AGATTCACTA TTCATACTGG TGCTGGAAAG ATCGTTCCTG	120
AAATACAAAG TGATGGGCAG GTAAAGGTTG ATATGGGCGA GCCTATCCTT TCTGGACTAG	180
ACATCCCCAC AAAACTGCTA GCTACCAAGA ACAAAGCTGT TGTTCAAGCT GAATTGGCAG	240
TTGAGGGCTT AACATGGCAT GTCACATGTG TTAGCATGGG AAACCCTCAC TGTGTCACAT	300

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TTGGTGCAAA TGAGTTAAAG GTATTGCAGG TCGACGATTT AAAACTTAGC GAAATTGGGC      360
CTAAATTTGA GCATCATGAA ATGTTTCCTG CTCGCACAAA CACAGAATTC GTACAGGTTT      420
TGTCTCGCTC ACACCTCAAA ATGCGGGTCT GGGAACGTGG TGCTGGAGCA ACTCTTGCCT      480
GTGGTACTGG TGCTTGTGCA GTGGTTGTTG CAGCTGTTCT TGAGGGTCGA GCTGAGCGGA      540
AATGTGTAGT TGATTTCCTT GCGGGGCCAT TGGAAATTGA GTGGAGGGAG GATGACAATC      600
ATGTTTACAT GACTGGTCCT GCAGAGGTCG TCTTTTATGG ATCTGTTGTT CACTAGGTAC      660
TGGGGACCAA GATAGAAGGG TTGGCTGCCA CTCAGAGCTT GTGAGATTGG TTATAGTATC      720
CATGAAACAG AGTGTTCCTG TACCAGTACA CTTGTTCAGA TATTCTTAAT TATGATTGCT      780
TGATTTGGGT AGCMGTAGAG GCTTCCTTTT GAAGCATTCT AGTGTTCMCC TTTTGTACTC      840
CTTTAGTTTG TCAGGTTTGA AACTACATG GGTAACATGT CYTCCCACC ATTTTCYGTG      900
TCTTTTCTTT GTAAGTGAAC GCCAATGCAG TTTTAGTATT GTTTTCTATA GATTTGTCTT      960
GATGCACTGG GCTTACTACT TATTTTCTGG TATGAATGCT GCCTATTTCC TG      1012

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: chp2.pk0008.h4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Leu Pro Glu Met Cys Gly Asn Gly Val Arg Cys Phe Ala Arg Phe Ile
1           5           10           15
Ala Glu Ile Glu Asn Leu Gln Gly Thr Asn Arg Phe Thr Ile His Thr
20           25           30
Gly Ala Gly Lys Ile Val Pro Glu Ile Gln Ser Asp Gly Gln Val Lys
35           40           45
Val Asp Met Gly Glu Pro Ile Leu Ser Gly Leu Asp Ile Pro Thr Lys
50           55           60
Leu Leu Ala Thr Lys Asn Lys Ala Val Val Gln Ala Glu Leu Ala Val
65           70           75           80
Glu Gly Leu Thr Trp His Val Thr Cys Val Ser Met Gly Asn Pro His
85           90           95
Cys Val Thr Phe Gly Ala Asn Glu Leu Lys Val Leu Gln Val Asp Asp
100          105          110
Leu Lys Leu Ser Glu Ile Gly Pro Lys Phe Glu His His Glu Met Phe
115          120          125
Pro Ala Arg Thr Asn Thr Glu Phe Val Gln Val Leu Ser Arg Ser His
130          135          140

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Leu Lys Met Arg Val Trp Glu Arg Gly Ala Gly Ala Thr Leu Ala Cys
 145 150 155 160
 Gly Thr Gly Ala Cys Ala Val Val Val Ala Ala Val Leu Glu Gly Arg
 165 170 175
 Ala Glu Arg Lys Cys Val Val Asp Leu Pro Gly Gly Pro Leu Glu Ile
 180 185 190
 Glu Trp Arg Glu Asp Asp Asn His Val Tyr Met Thr Gly Pro Ala Glu
 195 200 205
 Val Val Phe Tyr Gly Ser Val Val His
 210 215

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: rls48.pk0036.h10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGTATCCGGC GCCGACGGTG TGATCTTCGT CATGCCGGGG GTCAATGGCG CGGACTACAC 60
 CATGAGGATC TTCAACTCGG ACGGCAGTGA GCCGGAGATG TGTGGCAATG GAGTCCGTTG 120
 CTTTGCCCGG TTTATAGCTG AGCTTGAAAA CCTACAGGGA ACACATAGCT TCAA AATTC A 180
 CACTGGCGCT GGGCTAATCA TTCCTGAAAT ACAA AATGAT GGCAAGGTAA AGGTTGATAT 240
 GGGCCAGCCC ATTCTCTCTG GACCAGATAT TCCAACAAAA CTGCCATCCA CCAAGAATGA 300
 AGCCGTTGTC CAAGCTGATT TGGGCAGTTG ATGGCTCAAC ATGGCAAGTA ACCTGTGTGA 360
 GCATGGGCAA TCCACATTGT GTCACATTG GCACAAAGGA GCTCAAGGTT TTGCATGTTG 420
 ATGATTAAAG CTTAATGATA TTGGGGCCTA AATTCAGCAT CATGAAATGT TCCTGCCCCA 480
 C 481

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: rls48.pk0036.h10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Ser Gly Ala Asp Gly Val Ile Phe Val Met Pro Gly Val Asn Gly
 1 5 10 15

Ala Asp Tyr Thr Met Arg Ile Phe Asn Ser Asp Gly Ser Glu Pro Glu
 20 25 30
 Met Cys Gly Asn Gly Val Arg Cys Phe Ala Arg Phe Ile Ala Glu Leu
 35 40 45
 Glu Asn Leu Gln Gly Thr His Ser Phe Lys Ile His Thr Gly Ala Gly
 50 55 60
 Leu Ile Ile Pro Glu Ile Gln Asn Asp Gly Lys Val Lys Val Asp Met
 65 70 75 80
 Gly Gln Pro Ile Leu
 85

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCCCTTATT AAGCAGGGGT TTCGCGGCGC GAGACGGTGA CACTGGCAGA GTGGAATTC 60
 CGCCGCCATT CGAAGCTACA GCGATGGCCA TAACCGCCAC CATTTCGGTT CCCCTCACAT 120
 CCCCCAGTCG CCGCACTCTC ACCTCCGTCA ATAGCCTCTC TCCCCTTCT ACCCGATCCA 180
 CTTTGCCAC ACCGCAACGC ACTTTCAAT ACCCTAATTC GCGCCTCGTC GTGTCTTCCA 240
 TGAGACCGGA AACAGCCGTC AAAACTTCAT CCGCCTCCTT CCTCAACCGC AAGGAGTCCG 300
 GCTTCCTCCA TTCGCCAAG TACCACGGCC TCGGAAACGA CTTCGTTTTG ATTGACAATA 360
 GAGACTCCTC CGAGCCCAAG ATCAGTGCTG AGAAAGCGGT GCAACTGTGT GATCGGAACT 420
 TCGGCGTTGG AGCTGACGGA GTTATCTTTG TCTTGCTGG CATCAGTGGC ACCGATTATA 480
 CCATGAGGAT TTTTAACTCT GATGGTAGTG AGCCTGAGAT GTGTGGCAAT GGAGTTCGAT 540
 GCTTTGCCAA ATTTGTTTCT CAGCTTGAGA ATTTACATGG GAGGCATAGT TTTACCATTC 600
 ATACTGGTGC TGGTCTGATT ATTCCTGAAG TCTTGAGGA TGGAAATGTC AGAGTTGATA 660
 TGGGGGAGCC AGTTCTTAA GCCTTGATG TGCCTACTAA ATTACCTGCA AATAAGGATA 720
 ATGCTGTTGT TAAATCACAG CTAGTTGTAG ATGGAGTTAT TTGGCATGTG ACCTGTGTTA 780
 GCATGGGGAA TCCCACTGT GTAACCTTCA GTAGAGAAGG AAGCCAGAAT TTGCTTGTG 840
 ATGAATTGAA GCTAGCAGAA ATTGGGCCAA AATTTGAACA TCATGAGGTG TTCCCTGCAC 900
 GAACTAACAC AGAGTTTGTG CAAGTATTAT CTAACCTCTCA CTTGAAAATG CGTGTTTGGG 960
 AGCGGGGAGC AGGAGCAACC CTAGCCTGTG GAACTGGAGC TTGTGCTACT GTTGTTCAG 1020
 CAGTTCTTGA GGGTCGTGCT GGGAGGAATT GCACGGTTGA TCTACCTGGA GGGCCTCTTC 1080
 AGATTGAGTG GAGGGAGGAA GATAATCATG TTTATATGAC AGGCTCAGCC GATGTAGTTT 1140

ATTATGGTTC TTGCCCCCTT TGATATGTTG CCCCCATTGT TAAACCCAAT ATGGAATTAG 1200
 GAATTGGTGA ATAATATTTG TATGAGAGGT GGACTTTCTG CTTGTTCTTA ATATTTTGCC 1260
 ACGTCTTTAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A 1301

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Ile Thr Ala Thr Ile Ser Val Pro Leu Thr Ser Pro Ser Arg
 1 5 10 15
 Arg Thr Leu Thr Ser Val Asn Ser Leu Ser Pro Leu Ser Thr Arg Ser
 20 25 30
 Thr Leu Pro Thr Pro Gln Arg Thr Phe Lys Tyr Pro Asn Ser Arg Leu
 35 40 45
 Val Val Ser Ser Met Ser Thr Glu Thr Ala Val Lys Thr Ser Ser Ala
 50 55 60
 Ser Phe Leu Asn Arg Lys Glu Ser Gly Phe Leu His Phe Ala Lys Tyr
 65 70 75 80
 His Gly Leu Gly Asn Asp Phe Val Leu Ile Asp Asn Arg Asp Ser Ser
 85 90 95
 Glu Pro Lys Ile Ser Ala Glu Lys Ala Val Gln Leu Cys Asp Arg Asn
 100 105 110
 Phe Gly Val Gly Ala Asp Gly Val Ile Phe Val Leu Pro Gly Ile Ser
 115 120 125
 Gly Thr Asp Tyr Thr Met Arg Ile Phe Asn Ser Asp Gly Ser Glu Pro
 130 135 140
 Glu Met Cys Gly Asn Gly Val Arg Cys Phe Ala Lys Phe Val Ser Gln
 145 150 155 160
 Leu Glu Asn Leu His Gly Arg His Ser Phe Thr Ile His Thr Gly Ala
 165 170 175
 Gly Leu Ile Ile Pro Glu Val Leu Glu Asp Gly Asn Val Arg Val Asp
 180 185 190
 Met Gly Glu Pro Val Leu Lys Ala Leu Asp Val Pro Thr Lys Leu Pro
 195 200 205
 Ala Asn Lys Asp Asn Ala Val Val Lys Ser Gln Leu Val Val Asp Gly
 210 215 220
 Val Ile Trp His Val Thr Cys Val Ser Met Gly Asn Pro His Cys Val
 225 230 235 240
 Thr Phe Ser Arg Glu Gly Ser Gln Asn Leu Leu Val Asp Glu Leu Lys
 245 250 255

Leu Ala Glu Ile Gly Pro Lys Phe Glu His His Glu Val Phe Pro Ala
 260 265 270
 Arg Thr Asn Thr Glu Phe Val Gln Val Leu Ser Asn Ser His Leu Lys
 275 280 285
 Met Arg Val Trp Glu Arg Gly Ala Gly Ala Thr Leu Ala Cys Gly Thr
 290 295 300
 Gly Ala Cys Ala Thr Val Val Ala Ala Val Leu Glu Gly Arg Ala Gly
 305 310 315 320
 Arg Asn Cys Thr Val Asp Leu Pro Gly Gly Pro Leu Gln Ile Glu Trp
 325 330 335
 Arg Glu Glu Asp Asn His Val Tyr Met Thr Gly Ser Ala Asp Val Val
 340 345 350
 Tyr Tyr Gly Ser Leu Pro Leu
 355

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 602 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: wlm24.pk0030.g4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTCCACCGCC CCCTCCTCGG GCGGTCGCCT CCTCCGTCCG TTCTGTGGGA ATCCGCGCCC	60
CCGCCGCGCC GTCGCCTCGA TGGCCGTGTC CGCTCCCAAG TCGCCAGCCG CCGCCTCGTT	120
CCTCGAGCGC CGCGAGTCCG AGCGCGCGCT CCACTTCGTG AAGTACCAGG GCCTCGGCAA	180
CGACTTCATA ATGGTCGACA ACAGGGATTC GGCCGTACCG AAGGTGACAC CGGAGGAGGC	240
GGCGAAGCTA TGCGACCGAA ACTTTGGGTA TTGGGTGCTG ATGGCGTCAT CTTCGTCCTG	300
CCGGGGGTCA ACGGCGCGGA CTACACTATG AGGATATTCA ACTCCGATGG CAGCAACCGG	360
AATGTNTGGN ATGGATTTCGT TGCTTGCTCG CTTTATACGG AGTTGAAATC TACANGGAAA	420
CATACTTCAA AACAAAGGG GGCTGGATTA ATATCCTGAA ATANANACAT GNAAGTTANG	480
TNATATGGGC AACAACTTA TGGCANATTT CANAAAATGC ATCACAAGAT AACTTNTAAA	540
ACGATTGAAT TAGGCAANAG AANTACCGTT ATAGGAACCC ATGAANCTTG TNAAATTAAG	600
GT	602

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: wlm24.pk0030.g4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Ala Leu His Phe Val Lys Tyr Gln Gly Leu Gly Asn Asp Phe Ile Met
 1             5             10             15
Val Asp Asn Arg Asp Ser Ala Val Pro Lys Val Thr Pro Glu Ala
 20             25             30
Ala Lys Leu Cys Asp Arg Asn Phe Gly Xaa Gly Ala Asp Gly Val Ile
 35             40             45
Phe Val Leu Pro Gly Val Asn Gly Ala Asp Tyr Thr Met Arg Ile Phe
 50             55             60
Asn Ser Asp Gly Ser Asn Arg Asn Val Trp Xaa Gly Phe Val Ala Cys
 65             70             75             80

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Synechocystus sp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Met Ala Leu Ser Phe Ser Lys Tyr His Gly Leu Gly Asn Asp Phe Ile
 1             5             10             15
Leu Val Asp Asn Arg Gln Ser Thr Glu Pro Cys Leu Thr Pro Asp Gln
 20             25             30
Ala Gln Gln Leu Cys Asp Arg His Phe Gly Ile Gly Ala Asp Gly Val
 35             40             45
Ile Phe Ala Leu Pro Gly Gln Gly Gly Thr Asp Tyr Thr Met Arg Ile
 50             55             60
Phe Asn Ser Asp Gly Ser Glu Pro Glu Met Cys Gly Asn Gly Ile Arg
 65             70             75             80
Cys Leu Ala Lys Phe Leu Ala Asp Leu Glu Gly Val Glu Glu Lys Thr
 85             90             95
Tyr Arg Ile His Thr Leu Ala Gly Val Ile Thr Pro Gln Leu Leu Ala
100             105             110
Asp Gly Gln Val Lys Val Asp Met Gly Glu Pro Gln Leu Leu Ala Glu
115             120             125
Leu Ile Pro Thr Thr Leu Ala Pro Ala Gly Glu Lys Val Val Asp Leu
130             135             140
Pro Leu Ala Val Ala Gly Gln Thr Trp Ala Val Thr Cys Val Ser Met
145             150             155             160

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Gly Asn Pro His Cys Leu Thr Phe Val Asp Asp Val Asp Ser Leu Asn
 165 170 175
 Leu Thr Glu Ile Gly Pro Leu Phe Glu His His Pro Gln Phe Ser Gln
 180 185 190
 Arg Thr Asn Thr Glu Phe Ile Gln Val Leu Gly Ser Asp Arg Leu Lys
 195 200 205
 Met Arg Val Trp Glu Arg Gly Ala Gly Ile Thr Leu Ala Cys Gly Thr
 210 215 220
 Gly Ala Cys Ala Thr Val Val Ala Ala Val Leu Thr Gly Arg Gly Asp
 225 230 235 240
 Arg Arg Cys Thr Val Glu Leu Pro Gly Gly Asn Leu Glu Ile Glu Trp
 245 250 255
 Ser Ala Gln Asp Asn Arg Leu Tyr Met Thr Gly Pro Ala Gln Arg Val
 260 265 270
 Phe Ser Gly Gln Ala Glu Ile
 275

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: cc2.pk0031.c9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTCGGCTGCG CGTCCACGGG AGACACCTCC GCCGCGCTCT CGGCCTACTG CGCAGCCGCG	60
GGAATCCCCG CCATCGTGTT CCTGCCAGCG GACCGCATCT CGCTGCAGCA GCTCATCCAG	120
CCGATCGCCA ACGGCGCCAC CGTGCTCTCT CTAGACACTG ATTTTGATGG CTGCATGCGG	180
CTCATTCGCG AGGTCACTGC AGAGCTGCCA ATCTACCTTG CCAATTCGCT CAACCCGCTC	240
CGCCTTGAGG GGCAGAAGAC AGCGGCCATC GAGATATTGC AGCAGTTCAA TTGGCAGGTG	300
CCAGATTGGG TCATTGTTCC AGGAGGCAAT CTTGGAATA TCTATGCATT CTACAAGGGG	360
TTTGAGATGT GCCGCGTTCT TGGACTTGTT GATCGCGTGC CACGGCTTGT CTGCGCACAG	420
GCTGCAAATG CAAATCCATT GTACCGGTAC TACAAGTCAG GTTGACTGA GTTTGAGCCA	480
CAAAGTCCCG AGACTACATT TGCATCTGCG ATACAGATTG GTGATCCTGT ATCTGTTGAC	540
CGTGCGGTGG TCGCGTGAA GGCCACTGAC GGTATTGTGG AGGAGGCTAC AGAGGAGGAG	600
CTAATGGATG CAACGGCGCT TGCTGACCGC ACTGGGATGT TTGCTTGCCC ACATACTGGG	660
GTTGCACTTG CTGCTTTGTT TAAGCTTCAG GGTCAGCGTA TAATTGGCCC TAATGACCGC	720
ACTGTGGTTG TTAGCACAGC TCATGGGCTG AAGTTCACGC AGTCAAAGAT TGACTIONCAT	780

GACAAAAACA TCAAAGACAT GGTTTGCCAG TATGCTAATC CACCGATCAG TGTGAAGGCT 840
 GACTTTGGTT CTGTGATGGA TGTTCTCCAG AAAAATCTCA ATGGTAAGAT ATAAAGTTAT 900
 ATGATTAATT AACCTCCAA ACTGTTTTTT TTTGTTTTTT CGTCCAGGA ATTTTATTCC 960
 TGAGTCTTTC AACTTTGTTT GGTGAACATG GTATGGTGCT AAAATCTAGA CCTAATACCT 1020
 TGTAGTACTA GTTCTGGAGG CTCTTTTGGT TGTAGGTCGA AGTGGATAGA GCTGTTTCCTT 1080
 GTACTTTATC TGTTTCATGT AATATGAATA ATAAATTATG GTCTAAATAT TTGAATAAAA 1140
 AATCGTTTGG AATGACCCAC 1160

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: cc2.pk0031.c9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Gly Cys Ala Ser Thr Gly Asp Thr Ser Ala Ala Leu Ser Ala Tyr
 1 5 10 15
 Cys Ala Ala Ala Gly Ile Pro Ala Ile Val Phe Leu Pro Ala Asp Arg
 20 25 30
 Ile Ser Leu Gln Gln Leu Ile Gln Pro Ile Ala Asn Gly Ala Thr Val
 35 40 45
 Leu Ser Leu Asp Thr Asp Phe Asp Gly Cys Met Arg Leu Ile Arg Glu
 50 55 60
 Val Thr Ala Glu Leu Pro Ile Tyr Leu Ala Asn Ser Leu Asn Pro Leu
 65 70 75 80
 Arg Leu Glu Gly Gln Lys Thr Ala Ala Ile Glu Ile Leu Gln Gln Phe
 85 90 95
 Asn Trp Gln Val Pro Asp Trp Val Ile Val Pro Gly Gly Asn Leu Gly
 100 105 110
 Asn Ile Tyr Ala Phe Tyr Lys Gly Phe Glu Met Cys Arg Val Leu Gly
 115 120 125
 Leu Val Asp Arg Val Pro Arg Leu Val Cys Ala Gln Ala Ala Asn Ala
 130 135 140
 Asn Pro Leu Tyr Arg Tyr Tyr Lys Ser Gly Trp Thr Glu Phe Glu Pro
 145 150 155 160
 Gln Thr Ala Glu Thr Thr Phe Ala Ser Ala Ile Gln Ile Gly Asp Pro
 165 170 175
 Val Ser Val Asp Arg Ala Val Val Ala Leu Lys Ala Thr Asp Gly Ile
 180 185 190

Val Glu Glu Ala Thr Glu Glu Glu Leu Met Asp Ala Thr Ala Leu Ala
 195 200 205

Asp Arg Thr Gly Met Phe Ala Cys Pro His Thr Gly Val Ala Leu Ala
 210 215 220

Ala Leu Phe Lys Leu Gln Gly Gln Arg Ile Ile Gly Pro Asn Asp Arg
 225 230 235 240

Thr Val Val Val Ser Thr Ala His Gly Leu Lys Phe Thr Gln Ser Lys
 245 250 255

Ile Asp Tyr His Asp Lys Asn Ile Lys Asp Met Val Cys Gln Tyr Ala
 260 265 270

Asn Pro Pro Ile Ser Val Lys Ala Asp Phe Gly Ser Val Met Asp Val
 275 280 285

Leu Gln Lys Asn Leu Asn Gly Lys Ile
 290 295

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: csl.pk0058.g5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGCTTGCA AGTACTCCAA CCCGCCTGTG AGCGTGAAGG CTGACTTTGG CGCCGTGATG	60
GATGTGCTGA AGAAGAGGCT CAAGGGCAAG CTCTGAGCGC CTGTGCCTGG CTAATGCAAT	120
CAACTGATTG GAATGCAGTG GTTTCGTCGG TATCGGGGGG TCTTTTAGGC TTCAGAAATT	180
CTGTCTGGGT TAGACTATTT GTTTGTGGAG TTTAGCAGGA GAATGGCTAT CTCTCCTGCA	240
AGACTGGCGC TCTTTCTTGT GCTACGAATG TGTTACCATG GATAATAAGT GTAGTCGCTG	300
TCGGATTGAA TAATCAAAAA AAAAN	325

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: csl.pk0058.g5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Cys Lys Tyr Ser Asn Pro Pro Val Ser Val Lys Ala Asp Phe
1 5 10 15

Gly Ala Val Met Asp Val Leu Lys Lys Arg Leu Lys Gly Lys Leu
 20 25 30

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: rls72.pk0018.e7
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

ACACCCAACA CGCAGACTTG ACAGATTCTG CTACTACAAA TCCTGCATAT TTAACAGCGC      60
TGCAACTCGA CGATGGAGAA CGGTGCTGCA ACCAACGGGG CGTCGGAGAA GTCGCACTCT      120
CCTTCACAGA CCTACCTCTC CACAAGGGGA GACGATTATG GGCTCTCATT CGAGACCGTC      180
GTCCTCAAAG GTCTTGCGGC TGACGGGGGT CTTTTCCTGC CCGAGGAAGT GCCCGCGGCA      240
ACCGAGTGGC AAAGCTGGAA AGACCTGCCC TACACCGAGC TTGCCGTCOA GGTTCCTCAGC      300
TTGTACATCT CCCCCGCCGA GGTGCCGACG GAAGACCTCA GGGCGCTCGT CGAGCGCAGC      360
TACTCGACCT TCCGATCCAA GGAGGTTGTG CCGCTGGTGA AGCTGGAGGA CAACCTTCAC      420
CTGCTGGAGC TATTCCACGG CCCCACTAC TCGTTCAAGG ACTGCGCGCT GCAATTCCTT      480
GGTAACCTCN TCGAGTACTT TTGACTCNCA AGAACAAGGG AAAGGAGG      528
  
```

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: rls72.pk0018.e7
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Met Glu Asn Gly Ala Ala Thr Asn Gly Ala Ser Glu Lys Ser His Ser
1      5      10      15
Pro Ser Gln Thr Tyr Leu Ser Thr Arg Gly Asp Asp Tyr Gly Leu Ser
20     25     30
Phe Glu Thr Val Val Leu Lys Gly Leu Ala Ala Asp Gly Gly Leu Phe
35     40     45
Leu Pro Glu Glu Val Pro Ala Ala Thr Glu Trp Gln Ser Trp Lys Asp
50     55     60
Leu Pro Tyr Thr Glu Leu Ala Val Lys Val Leu Ser Leu Tyr Ile Ser
65     70     75     80
  
```

Pro Ala Glu Val Pro Thr Glu Asp Leu Arg Ala Leu Val Glu Arg Ser
 85 90 95
 Tyr Ser Thr Phe Arg Ser Lys Glu Val Val Pro Leu Val Lys Leu Glu
 100 105 110
 Asp Asn Leu His Leu Leu Glu Leu Phe His Gly Pro Asn Tyr Ser Phe
 115 120 125
 Lys Asp Cys Ala Leu Gln Phe Leu Gly Asn Leu Xaa Glu Tyr Phe
 130 135 140

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 571 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: sel.06a03

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATGCAATG GTGCAGGCTG ATTCCACTGG AATGTTTCATA TGTCCACACA CTGGGGTGGC	60
TCTGGCGGCG CTTATTAAGC TGAGGAATCG TGGGGTTATC GGTGCCGGTG AGAGGGTTGT	120
GGTGGTGAGC ACTGCACATG GATTGAAGTT TGCACAGAGC AAGATTGATT ATCATTCTGG	180
GCTCATTCCT GGAATGGGCC GCTATGCTAA CCCGCTGGTT TCGGTTAAGG CGGATTTTGG	240
ATCGGTCATG GATGTTCTCA AGGATTCTTG CACAACAAGT CCCCCGACTT TAACAAGTCT	300
TGACGTTGCC AAGTAAGTTT TAGTTCGGGG TTTTCTCTGA TTAAAGATGT TTTTAAACAT	360
GTTTGTGTNC ACTTTCGGTC GTTATTATGG ATTTGTAAGA TTGGGCCCAA GTATTCGAGG	420
GTTTGATTTC AAACAACATG CTTCTGGTGA CGCAATGCAA ATTTGCGNGC ATAACATCAT	480
TGTCGAAGAT GGATCNCGAC CGATGAAACT GTGTGGCAAG TAATGAGAAG AAAATAGGGC	540
ACTTGATACAG AGATTTNAAA GNTTAATTTC N	571

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: sel.06a03

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asp Ala Met Val Gln Ala Asp Ser Thr Gly Met Phe Ile Cys Pro His	
1 5 10 15	

Thr Gly Val Ala Leu Ala Ala Leu Ile Lys Leu Arg Asn Arg Gly Val
 20 25 30
 Ile Gly Ala Gly Glu Arg Val Val Val Val Ser Thr Ala His Gly Leu
 35 40 45
 Lys Phe Ala Gln Ser Lys Ile Asp Tyr His Ser Gly Leu Ile Pro Gly
 50 55 60
 Met Gly Arg Tyr Ala Asn Pro Leu Val Ser Val Lys Ala Asp Phe Gly
 65 70 75 80
 Ser Val Met Asp Val Leu Lys Asp Ser Cys Thr Thr Ser Pro Pro Thr
 85 90 95
 Leu Thr Ser Leu Asp Val Ala Lys
 100

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2191 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: srl.pk0003.f6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCTTCCTCTT CTCTGTTTCA GTCTCTCCCT TTCTCTCTCC AACCTCTAA ACCCTACGCG 60
 CCTCCCAAAC CCGCCGCCCA CTTGTTGTC CGCGCCAAT CCCCCCTCAC TCAGAACAAC 120
 AACTCTCTCT CCAAGCATCG CCGCCCCGCC GACGAGAACA TCCGCGACGA GGCCCGCCGC 180
 ATCAATGCGC CCCACGACCA CCACCTCTTC TCGGCCAAGT ACGTCCCCTT CAACGCCGAC 240
 TCCTCTCTCT CCTCTCCAC GGAGTCTTAC TCGCTCGACG AGATCGTCTA CCGCTCCCAA 300
 TCCGGCGGCC TCCTGGACGT CCAGCACGAC ATGGATGCCC TCAAGCGTTT CGACGGCGAG 360
 TACTGGCGCA ACCTCTTCGA CTCGCGCGTG GGCAAACCA CCTGGCCTTA CGGCTCCGGC 420
 GTCTGGAGCA AAAAGAATG GGTCTCCCC GAGATCCACG ACGACGATAT CGTCTCCGCC 480
 TTCGAGGGTA ACTCCAACCT CTTCTGGGCC GAGCGTTTCG GCAAACAGTT CCTCGGCATG 540
 AACGATTTGT GGGTCAAACA CTGCGGAATC AGCCACACGG GCAGCTTCAA GGATCTCGGC 600
 ATGACCGTCC TCGTCAGCCA GGTCAATCGC TTGAGAAAAA TGAACGCCC CGTCGTCGGT 660
 GTTGGTTGCG CCTCCACCGG TGACACATCG GCCGCTTTAT CCGCCTATTG CGCTTCCGCT 720
 GCCATTCTT CCATTGTGTT TTTGCTGCT AATAAAATCT CTCTGCCCA ACTTGTTGAG 780
 CCTATTGCCA ATGGAGCCTT TGTGTTGAGT ATCGACACTG ATTTTGATGG TGCAATGCAG 840
 TTGATCAGAG AAGTCACTGC TGAATTGCCT ATTTATTTGG CTAACCTCTCT CAACAGTTTG 900
 AAGTTGGAAG GGCAGAAAAC TGCTGCTATT GAGATTCTGC AGCAGTTTGA TTGGCAGGTT 960
 CCTGATTGGG TCATTGTGCC TGGAAGCAAC CTTGGCAACA TTTATGCCTT TTACAAAGGG 1020

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TTTAAGATGT TTCAAGAGCT TGGGCTTGTG GATAAGATTC CAAGGCTTGT TTGTGCTCAG 1080
GCTGCCAATG CTGATCCTTT GTATTTGTAC TTTAAATCCG GGTGGAAGGA GTTTAAGCCT 1140
GTGAAGTCGA GCACTACATT TGCTTCTGCC ATTCAAATTG GTGATCCTGT TTCCATTGAC 1200
AGGGCGGTTC ACGCGCTAAA GAGTTGCGAT GGGATTGTGG AGGAGGCCAC GGAGGAGGAG 1260
TTGATGGATG CTACAGCGCA GCGGATTCT ACTGGGATGT TTATTGCCC CCACACCGGG 1320
GTTGCTTTAA CTGCATTGTT TAAGCTCAGG AACAGCGGGG TTATTAAGGC CACTGATAGG 1380
ACTGTGGTGG TTAGCACTGC TCATGGCTTG AAGTTCCTC AGTCCAAGAT TGATTACCAT 1440
TCTAAGGACA TCAAGGACAT GGCTTGCCGC TATGCTAACC CGCCCATGCA AGTGAAGGCA 1500
GACTTTGGCT CGGTTATGGA TGTTTGAAG ACGTATTTGC AGAGTAAGGC TCATTAGGTT 1560
AGCATTGCAA GTTTTGCTCC TCCTGAGTTT GCTCATTATT TACTTACTTT TAGGCACTAC 1620
TGCTGTATTG TCTTTTCTAT GAGCTAGGTT TGAGTGTTGT AATAATTGTC TTGCTGCATT 1680
ATGTATGCCG TCTAGTGTT CATATTGGGC ATCATCCTTA GTATTTGTTG TAGATTTTCT 1740
TTGCTGAGCA TTTGATATAA TAGCTCAAGT AGGAAAATGA ATTGGGTACT ATGAGGAATG 1800
CATATCATTG GCTTGTATT ACTGGATTCC AGACCACCCC AAAAGAAAAT AATCCAAAA 1860
AATATAATTA GAACAAATTT CGTCCTTGTT ATGCTGTTGG CATTAGCTC AGTGTGGGTA 1920
TTACCAAGCA ACTCGAAATC AAGAGAAAAA AAAATTGACA GCAAAGGAGC TGCATTGTTG 1980
GACTGAGTCA CATCACTTCA TTGCTATGTC GTCATATTTC GTTGAATTAC GGAAGGCAG 2040
CATGCACAGC AATATGCAGC GATTAAGTGA AGCCACACCG CACACATTGA AGTAGTAGTC 2100
AATTTAGACA CTCCATCTTG TACTTTCTAC AAAAATGAAT TTTTCTTAGC CATTAGTAT 2160
AATATTTTAT TCTAAAAAAA AAAAAAAAAA A 2191

```

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 518 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: srl.pk0003.f6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Ala Ser Ser Ser Leu Phe Gln Ser Leu Pro Phe Ser Leu Gln Thr Ser
1           5           10           15
Lys Pro Tyr Ala Pro Pro Lys Pro Ala Ala His Phe Val Val Arg Ala
20           25           30
Gln Ser Pro Leu Thr Gln Asn Asn Asn Ser Ser Ser Lys His Arg Arg
35           40           45

```

Pro Ala Asp Glu Asn Ile Arg Asp Glu Ala Arg Arg Ile Asn Ala Pro
 50 55 60
 His Asp His His Leu Phe Ser Ala Lys Tyr Val Pro Phe Asn Ala Asp
 65 70 75 80
 Ser Ser Ser Ser Ser Ser Thr Glu Ser Tyr Ser Leu Asp Glu Ile Val
 85 90 95
 Tyr Arg Ser Gln Ser Gly Gly Leu Leu Asp Val Gln His Asp Met Asp
 100 105 110
 Ala Leu Lys Arg Phe Asp Gly Glu Tyr Trp Arg Asn Leu Phe Asp Ser
 115 120 125
 Arg Val Gly Lys Thr Thr Trp Pro Tyr Gly Ser Gly Val Trp Ser Lys
 130 135 140
 Lys Glu Trp Val Leu Pro Glu Ile His Asp Asp Asp Ile Val Ser Ala
 145 150 155 160
 Phe Glu Gly Asn Ser Asn Leu Phe Trp Ala Glu Arg Phe Gly Lys Gln
 165 170 175
 Phe Leu Gly Met Asn Asp Leu Trp Val Lys His Cys Gly Ile Ser His
 180 185 190
 Thr Gly Ser Phe Lys Asp Leu Gly Met Thr Val Leu Val Ser Gln Val
 195 200 205
 Asn Arg Leu Arg Lys Met Asn Arg Pro Val Val Gly Val Gly Cys Ala
 210 215 220
 Ser Thr Gly Asp Thr Ser Ala Ala Leu Ser Ala Tyr Cys Ala Ser Ala
 225 230 235 240
 Ala Ile Pro Ser Ile Val Phe Leu Pro Ala Asn Lys Ile Ser Leu Ala
 245 250 255
 Gln Leu Val Gln Pro Ile Ala Asn Gly Ala Phe Val Leu Ser Ile Asp
 260 265 270
 Thr Asp Phe Asp Gly Cys Met Gln Leu Ile Arg Glu Val Thr Ala Glu
 275 280 285
 Leu Pro Ile Tyr Leu Ala Asn Ser Leu Asn Ser Leu Lys Leu Glu Gly
 290 295 300
 Gln Lys Thr Ala Ala Ile Glu Ile Leu Gln Gln Phe Asp Trp Gln Val
 305 310 315 320
 Pro Asp Trp Val Ile Val Pro Gly Ser Asn Leu Gly Asn Ile Tyr Ala
 325 330 335
 Phe Tyr Lys Gly Phe Lys Met Phe Gln Glu Leu Gly Leu Val Asp Lys
 340 345 350
 Ile Pro Arg Leu Val Cys Ala Gln Ala Ala Asn Ala Asp Pro Leu Tyr
 355 360 365
 Leu Tyr Phe Lys Ser Gly Trp Lys Glu Phe Lys Pro Val Lys Ser Ser
 370 375 380
 Thr Thr Phe Ala Ser Ala Ile Gln Ile Gly Asp Pro Val Ser Ile Asp
 385 390 395 400

Arg Ala Val His Ala Leu Lys Ser Cys Asp Gly Ile Val Glu Glu Ala
 405 410 415

Thr Glu Glu Glu Leu Met Asp Ala Thr Ala Gln Ala Asp Ser Thr Gly
 420 425 430

Met Phe Ile Cys Pro His Thr Gly Val Ala Leu Thr Ala Leu Phe Lys
 435 440 445

Leu Arg Asn Ser Gly Val Ile Lys Ala Thr Asp Arg Thr Val Val Val
 450 455 460

Ser Thr Ala His Gly Leu Lys Phe Thr Gln Ser Lys Ile Asp Tyr His
 465 470 475 480

Ser Lys Asp Ile Lys Asp Met Ala Cys Arg Tyr Ala Asn Pro Pro Met
 485 490 495

Gln Val Lys Ala Asp Phe Gly Ser Val Met Asp Val Leu Lys Thr Tyr
 500 505 510

Leu Gln Ser Lys Ala His
 515

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 643 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: wr1.pk0085.h2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTCATCCAG CCCATCGCCA ACGGCGCCAC GGTGCTCTCG CTTGACACGG ATTTGACGG	60
ATGCATGCGG CTTATCAGGG AGGTGACAGC TGAGCTGCCC ATATACCTCG CAAACTCACT	120
CAACTCGCTT CCGGCTGGAG GGGCAGAAGA CTGCAGCCAT CCGAGATATT GCAACANTCA	180
ATTGGCAGGT GCCCGGACTG GGTACATCC CAAGGAGGCA ATCTGGGGGA ACATTTTATG	240
CTTTCCTACA AGGATTTNAA TTTCCGTGTC CTTNGCTAGT TGATTNCCTT CCNACTCCTT	300
GTTANTNCAA NAGGCCGCCA ACGCAAACCC ACTGTACCCG TACTACAATC CTGGGGTGAC	360
TGATTTCCAT CCACTTGNTT GCCGGGACAA TTTNCATCCN GCAACAATTT GGGGATTCCA	420
TATCNATTAC CNTCGGTTTT TTCNCCCTNA AAGGACNNAT GATTNTCCNA GGAACTCCNN	480
AGGNGGATCA AGGATCCAAA GGCTTTCTAC TCACTGGAAN TTGCTTCCCA ANACGGGGTT	540
CACTNCCGCC CGTTAAACCC NTGACAAGTA TAATGGACAA CACNCCGGGG TNTATNACAA	600
CGGCAANTTN AAANCAAGTT NATCATTAGA ACNGGAANTT NCC	643

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: wr1.pk0085.h2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Leu Ile Gln Pro  Ile Ala Asn Gly Ala Thr Val Leu Ser Leu Asp Thr
1              5              10              15
Asp Phe Asp Gly Cys Met Arg Leu Ile Arg Glu Val Thr Ala Glu Leu
20            25            30
Pro Ile Tyr Leu Ala Asn Ser Leu Asn Ser Leu Xaa Leu Glu Gly Gln
35            40            45
Lys Thr Ala Ala Ile Arg Asp Ile Ala Thr Xaa Asn Trp Gln Val Pro
50            55            60
Gly Leu Gly His Ile Pro Arg Arg Gln Ser Xaa Thr Phe Tyr Ala Phe
65            70            75            80
Leu Gln Gly Phe

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 525 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Arabidopsis thaliana

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Leu Ser Ser Cys Leu Phe Asn Ala Ser Val Ser Ser Leu Asn Pro Lys
1              5              10              15
Gln Asp Pro Ile Arg Arg His Arg Ser Thr Ser Leu Leu Arg His Arg
20            25            30
Pro Val Val Ile Ser Cys Thr Ala Asp Gly Asn Asn Ile Lys Ala Pro
35            40            45
Ile Glu Thr Ala Val Lys Pro Pro His Arg Thr Glu Asp Asn Ile Arg
50            55            60
Asp Glu Ala Arg Arg Asn Arg Ser Asn Ala Val Asn Pro Phe Ser Ala
65            70            75            80
Lys Tyr Val Pro Phe Asn Ala Ala Pro Gly Ser Thr Glu Ser Tyr Ser
85            90            95
Leu Asp Glu Ile Val Tyr Arg Ser Arg Ser Gly Gly Leu Leu Asp Val
100           105           110
Glu His Asp Met Glu Ala Leu Lys Arg Phe Asp Gly Ala Tyr Trp Arg
115           120           125

```

Asp Leu Phe Asp Ser Arg Val Gly Lys Ser Thr Trp Pro Tyr Gly Ser
 130 135 140
 Gly Val Trp Ser Lys Lys Glu Trp Val Leu Pro Glu Ile Asp Asp Asp
 145 150 155 160
 Asp Ile Val Ser Ala Phe Glu Gly Asn Ser Asn Leu Phe Trp Ala Glu
 165 170 175
 Arg Phe Gly Lys Gln Phe Leu Gly Met Asn Asp Leu Trp Val Lys His
 180 185 190
 Cys Gly Ile Ser His Thr Gly Ser Phe Lys Asp Leu Gly Met Thr Val
 195 200 205
 Leu Val Ser Gln Val Asn Arg Leu Arg Lys Met Lys Arg Pro Val Val
 210 215 220
 Gly Val Gly Cys Ala Ser Thr Gly Asp Thr Ser Ala Ala Leu Ser Ala
 225 230 235 240
 Tyr Cys Ala Ser Ala Gly Ile Pro Ser Ile Val Phe Leu Pro Ala Asn
 245 250 255
 Lys Ile Ser Met Ala Gln Leu Val Gln Pro Ile Ala Asn Gly Ala Phe
 260 265 270
 Val Leu Ser Ile Asp Thr Asp Phe Asp Gly Cys Met Lys Leu Ile Arg
 275 280 285
 Glu Ile Thr Ala Glu Leu Pro Ile Tyr Leu Ala Asn Ser Leu Asn Ser
 290 295 300
 Leu Arg Leu Glu Gly Gln Lys Thr Ala Ala Ile Glu Ile Leu Gln Gln
 305 310 315 320
 Phe Asp Trp Gln Val Pro Asp Trp Val Ile Val Pro Gly Gly Asn Leu
 325 330 335
 Gly Asn Ile Tyr Ala Phe Tyr Lys Gly Phe Lys Met Cys Gln Glu Leu
 340 345 350
 Gly Leu Val Asp Arg Ile Pro Arg Met Val Cys Ala Gln Ala Ala Asn
 355 360 365
 Ala Asn Pro Leu Tyr Leu His Tyr Lys Ser Gly Trp Lys Asp Phe Lys
 370 375 380
 Pro Met Thr Ala Ser Thr Thr Phe Ala Ser Ala Ile Gln Ile Gly Asp
 385 390 395 400
 Pro Val Ser Ile Asp Arg Ala Val Tyr Ala Leu Lys Lys Cys Asn Gly
 405 410 415
 Ile Val Glu Glu Ala Thr Glu Glu Glu Leu Met Asp Ala Met Ala Gln
 420 425 430
 Ala Asp Ser Thr Gly Met Phe Ile Cys Pro His Thr Gly Val Ala Leu
 435 440 445
 Thr Ala Leu Phe Lys Leu Arg Asn Gln Gly Val Ile Ala Pro Thr Asp
 450 455 460
 Arg Thr Val Val Val Ser Thr Ala His Gly Leu Lys Phe Thr Gln Ser
 465 470 475 480

Lys Ile Asp Tyr His Ser Asn Ala Ile Pro Asp Met Ala Cys Arg Phe
 485 490 495

Ser Asn Pro Pro Val Asp Val Lys Ala Asp Phe Gly Ala Val Met Asp
 500 505 510

Val Leu Lys Ser Tyr Leu Gly Ser Asn Thr Leu Thr Ser
 515 520 525

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1478 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: cen1.pk0064.f4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAACAGTGGT CCTTGAGGGG GACTCATATG ATGAAGCTCA GTCATATGCA AAATTGCGTT	60
GCCAGCAGGA AGGCCGCACA TTTGTACCTC CTTTGACCA TCCTGATGTC ATCACTGGAC	120
AAGGAACATAT CGGCATGGAA ATTGTTAGGC AGCTGCAAGG TCCACTGCAT GCAATATTTG	180
TACCTGTTGG AGGTGGTGGG TTAATTGCTG GAATTGCTGC CTATGTAAAA CGGGTTCGCC	240
CAGAGGTGAA AATAATTGGA GTGGAACCTT CAGATGCAAA TGCAATGGCA TTATCCTTGT	300
GTCATGGTAA GAGGGTCATG TTGGAGCATG TTGGTGGGTT TGCTGATGGT GTAGCTGTCA	360
AAGCTGTTGG GGAAGAAACA TTTCGCCTGT GCAGAGAGCT AGTAGATGGC ATTGTTATGG	420
TCAGTCGAGA TGCTATTTGT GCTTCAATAA AGGATATGTT TGAGGAGAAA AGAAGTATCC	480
TTGAACCTGC TGGTGCCCTT GCATTGGCTG GGGCTGAAGC CTACTGCAAA TACTATAACT	540
TGAAAGGAGA AACTGTGGTT GCAATAACTA GTGGGGCAAA TATGAACTTT GATCGACTTA	600
GACTAGTAAC CGAGCTAGCT GATGTTGGCC GAAACGGGA AGCAGTGTTA GCTACATTTT	660
TGCCAGAGCG GCAGGGAAGC TTCAAAAAAT TCACAGAATT GGTGGCAGG ATGAATATTA	720
CTGAATTCAA ATACAGATAC GATTCTAATG CAAAGATGC CCTTGTCTT TACAGTGTG	780
GCATCTACAC TGACAATGAG CTTGGAGCAA TGATGGATCG CATGGAATCT GCGAACTGA	840
GGACTGTTAA CCTTACTGAC AATGATTTGG CAAAGGACCA CCTTAGATAC TTTATTGGAG	900
GAAGATCAGA AATAAAAGAT GAACTGGTTT ACCGGTTCAT TTTCCCGGAA AGGCCTGGGG	960
CCCTTATGAA ATTTTGGAC ACGTTTAGTC CTCGTTGGAA CATCAGCCTT TTCCATTACC	1020
GTGCACAGGG TGAAGCTGGA GCAATGTAT TAGTTGGTAT ACAAGTGCCG CCAGCAGAAT	1080
TTGATGAATT CAAGAGTCAT GCCAACAATC TTGGGTACGA GTACATGTCA GAGCACAACA	1140
ATGAGATATA CCGGTTGCTG TTGCGTGACC CAAAGGTCTA ATGTATATGC CTTTGCTCCC	1200
ATAATAAGTT GGTGACACTT TTCAAGGAAG ATTTTGCTCC AAGGTAGAAG TTGCGAGTTT	1260

CTTCAAGTTG AAATGAAGCC ATCACCAAAT GTAGCTTCGG TGTGCCATCT GTTTACTCAG 1320
 TTAGATCATG TAGTGTATCA GTTGTGTATC TTTGTTGTTG TGCTTCGTGA TCTCAATTTA 1380
 TTGCTTTGTG CACCTAGAGG TTGTCAAATA ATGATAACCG ATATGTTATC TAAATATCTA 1440
 ATAATGATTA TGTGATTGTG ATTAATAAGG GGGGGCCC 1478

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: cen1.pk0064.f4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Thr Val Val Leu Glu Gly Asp Ser Tyr Asp Glu Ala Gln Ser Tyr Ala
 1 5 10 15
 Lys Leu Arg Cys Gln Gln Glu Gly Arg Thr Phe Val Pro Pro Phe Asp
 20 25 30
 His Pro Asp Val Ile Thr Gly Gln Gly Thr Ile Gly Met Glu Ile Val
 35 40 45
 Arg Gln Leu Gln Gly Pro Leu His Ala Ile Phe Val Pro Val Gly Gly
 50 55 60
 Gly Gly Leu Ile Ala Gly Ile Ala Ala Tyr Val Lys Arg Val Arg Pro
 65 70 75 80
 Glu Val Lys Ile Ile Gly Val Glu Pro Ser Asp Ala Asn Ala Met Ala
 85 90 95
 Leu Ser Leu Cys His Gly Lys Arg Val Met Leu Glu His Val Gly Gly
 100 105 110
 Phe Ala Asp Gly Val Ala Val Lys Ala Val Gly Glu Glu Thr Phe Arg
 115 120 125
 Leu Cys Arg Glu Leu Val Asp Gly Ile Val Met Val Ser Arg Asp Ala
 130 135 140
 Ile Cys Ala Ser Ile Lys Asp Met Phe Glu Glu Lys Arg Ser Ile Leu
 145 150 155 160
 Glu Pro Ala Gly Ala Leu Ala Leu Ala Gly Ala Glu Ala Tyr Cys Lys
 165 170 175
 Tyr Tyr Asn Leu Lys Gly Glu Thr Val Val Ala Ile Thr Ser Gly Ala
 180 185 190
 Asn Met Asn Phe Asp Arg Leu Arg Leu Val Thr Glu Leu Ala Asp Val
 195 200 205
 Gly Arg Lys Arg Glu Ala Val Leu Ala Thr Phe Leu Pro Glu Arg Gln
 210 215 220

Gly Ser Phe Lys Lys Phe Thr Glu Leu Val Gly Arg Met Asn Ile Thr
 225 230 235 240
 Glu Phe Lys Tyr Arg Tyr Asp Ser Asn Ala Lys Asp Ala Leu Val Leu
 245 250 255
 Tyr Ser Val Gly Ile Tyr Thr Asp Asn Glu Leu Gly Ala Met Met Asp
 260 265 270
 Arg Met Glu Ser Ala Lys Leu Arg Thr Val Asn Leu Thr Asp Asn Asp
 275 280 285
 Leu Ala Lys Asp His Leu Arg Tyr Phe Ile Gly Gly Arg Ser Glu Ile
 290 295 300
 Lys Asp Glu Leu Val Tyr Arg Phe Ile Phe Pro Glu Arg Pro Gly Ala
 305 310 315 320
 Leu Met Lys Phe Leu Asp Thr Phe Ser Pro Arg Trp Asn Ile Ser Leu
 325 330 335
 Phe His Tyr Arg Ala Gln Gly Glu Ala Gly Ala Asn Val Leu Val Gly
 340 345 350
 Ile Gln Val Pro Pro Ala Glu Phe Asp Glu Phe Lys Ser His Ala Asn
 355 360 365
 Asn Leu Gly Tyr Glu Tyr Met Ser Glu His Asn Asn Glu Ile Tyr Arg
 370 375 380
 Leu Leu Leu Arg Asp Pro Lys Val
 385 390

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 728 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: sf11.pk0055.h7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAATATTGT AGCAATAACC AGTGGAGCAA ACATGAATTT TGATAAACTT CGGGTTGTAA	60
CTGAACTTGC TAATGTTGGT CGTAAACAAG AGGCTGTGCT GGCAACTGTT ATGGCAGAGG	120
AGCCTGGCAG TTTCAAACAA TTTTGTGAAT TGGTGGGGCA GATGAACATA ACAGAATTCA	180
AATACAGATA TAACTCAAAT GAGAAGGCAG TTGTCCTTTA CAGTGTGGG GTTCACACAA	240
TCTCCGAACT AAGAGCAATG CAGGAGAGGA TGAATCTTC TCAGCTCAA ACTTACAATC	300
TCACAGAAAG TGAATTGGTG AAAGACCACT TGCCTTACTT GATGGGAGGC CGATCAAACG	360
TTCAGAATGA GGTCTTTGTC GTCTCACCTT TCCAAGAAAG ACTGGTGCTT TGATGAAATT	420
TTTGGACCTT TCAGTCCACG TTGGGATATT AGTTTATCCA TTACCGAGGG GAGGTGAAAC	480
TGGAGCAAAC TGCTAGTTGG NTACAGGTAC CAAAATGAGA TAGATGAGTC CATGATCGTG	540

CTAACAACT GGATATGATT ATAAGTGGNA ATATGTGATG NCTCAGCTCA ATCNCGATGG 600
 GGNTTAAGCA CTGCATATGG GNATTAGGGG NAGNTACANT TAAATTCACG GCCTCAAGNT 660
 AAGCATANTN TAGGAACTAG CTTTACAGGG GGCTACNANT TAACCGNGTA TTTTTTTTGA 720
 GATGANNG 728

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: sf11.pk0055.h7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Asn Ile Val Ala Ile Thr Ser Gly Ala Asn Met Asn Phe Asp Lys Leu
 1 5 10 15
 Arg Val Val Thr Glu Leu Ala Asn Val Gly Arg Lys Gln Glu Ala Val
 20 25 30
 Leu Ala Thr Val Met Ala Glu Glu Pro Gly Ser Phe Lys Gln Phe Cys
 35 40 45
 Glu Leu Val Gly Gln Met Asn Ile Thr Glu Phe Lys Tyr Arg Tyr Asn
 50 55 60
 Ser Asn Glu Lys Ala Val Val Leu Tyr Ser Val Gly Val His Thr Ile
 65 70 75 80
 Ser Glu Leu Arg Ala Met Gln Glu Arg Met Glu Ser Ser Gln Leu Lys
 85 90 95
 Thr Tyr Asn Leu Thr Glu Ser Asp Leu Val Lys Asp His Leu Arg Tyr
 100 105 110
 Leu Met Gly Gly Arg Ser Asn Val Gln Asn Glu Val Phe Val Val Ser
 115 120 125
 Pro Xaa Pro Arg Lys Thr Gly Ala Leu Met Lys Phe Leu Asp Xaa Phe
 130 135 140
 Ser Pro Arg Trp Asp Ile Ser Leu
 145 150

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 572 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: sre.pk0044.f3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

AAAGACCTGG TGCTTTGATG AAATTTTGG ACCCCTTCAG TCCACGTTGG AATATCAGTT      60
TATTCCATTA CCGAGGGGAG GGTGAACTG GAGCAAATGT GCTAGTTGGA ATACAGGTAC      120
CCAAAAGTGA GATGGATGAG TTCCACGATC GTCCAACAA ACTTGATAT GATTATAAAG      180
TGGTGAATAA TGATGATGAC TTCCAGCTTC TAATGCACTG ATGATGGTTT TAGGCACTTG      240
CCATTATTGT GTATTTTAGT CAACAAGTTT GCCATATTTA ATATTTCCAC GGTCGTTTCT      300
AAAAGTTGGA TGGGGAAAAA AGGTGGAAAG GAAGTGGCCT TCAGACATGT CATTAGTTGA      360
TTAGAGGAAC AACTAGTTCT TTTTACCTAA TCGGCGTCT TATTACATT TTTATAATCT      420
GTAATTTATG TTTTTTTGTT GTTGTTAACA TTGGAATCTT ATAATGTTGT TGCCTGGTCT      480
TTTGTGTCTG TAATATAAGT GTCTTCAAAA GGTGTTTGC TAAATTTTCAG CAGCCTAAAA      540
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                                     572

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(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: sre.pk0044.f3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

Arg Pro Gly Ala Leu Met Lys Phe Leu Asp Pro Phe Ser Pro Arg Trp
1          5          10          15
Asn Ile Ser Leu Phe His Tyr Arg Gly Glu Gly Glu Thr Gly Ala Asn
20        25        30
Val Leu Val Gly Ile Gln Val Pro Lys Ser Glu Met Asp Glu Phe His
35        40        45
Asp Arg Ala Asn Lys Leu Gly Tyr Asp Tyr Lys Val Val Asn Asn Asp
50        55        60
Asp Asp Phe Gln Leu Leu Met His
65        70

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(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 507 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Burkholderia capacia

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Ser His Asp Tyr Leu Lys Lys Ile Leu Thr Ala Arg Val Tyr
 1 5 10 15

Asp Val Ala Phe Glu Thr Glu Leu Glu Pro Ala Arg Asn Leu Ser Ala
 20 25 30

Arg Leu Arg Asn Pro Val Tyr Leu Lys Arg Glu Asp Asn Gln Pro Val
 35 40 45

Phe Ser Phe Lys Leu Arg Gly Ala Tyr Asn Lys Met Ala His Ile Pro
 50 55 60

Ala Asp Ala Leu Ala Arg Gly Val Ile Thr Ala Ser Ala Gly Asn His
 65 70 75 80

Ala Gln Gly Val Ala Phe Ser Ala Ala Arg Met Gly Val Lys Ala Val
 85 90 95

Ile Val Val Pro Val Thr Thr Pro Gln Val Lys Val Asp Ala Val Arg
 100 105 110

Ala His Gly Gly Pro Gly Val Glu Val Ile Gln Ala Gly Glu Ser Tyr
 115 120 125

Ser Asp Ala Tyr Ala His Ala Leu Lys Val Gln Glu Glu Arg Gly Leu
 130 135 140

Thr Phe Val His Pro Phe Asp Asp Pro Tyr Val Ile Ala Gly Gln Gly
 145 150 155 160

Thr Ile Ala Met Glu Ile Leu Arg Gln His Gln Gly Pro Ile His Ala
 165 170 175

Ile Phe Val Pro Ile Gly Gly Gly Gly Leu Ala Ala Gly Val Ala Ala
 180 185 190

Tyr Val Lys Ala Val Arg Pro Glu Ile Lys Val Ile Gly Val Gln Ala
 195 200 205

Glu Asp Ser Cys Ala Met Ala Gln Ser Leu Gln Ala Gly Lys Arg Val
 210 215 220

Glu Leu Ala Glu Val Gly Leu Phe Ala Asp Gly Thr Ala Val Lys Leu
 225 230 235 240

Val Gly Glu Glu Thr Phe Arg Leu Cys Lys Glu Tyr Leu Asp Gly Val
 245 250 255

Val Thr Val Asp Thr Asp Ala Leu Cys Ala Ala Ile Lys Asp Val Phe
 260 265 270

Gln Asp Thr Arg Ser Val Leu Glu Pro Ser Gly Ala Leu Ala Val Ala
 275 280 285

Gly Ala Lys Leu Tyr Ala Glu Arg Glu Gly Ile Glu Asn Gln Thr Leu
 290 295 300

Val Ala Val Thr Ser Gly Ala Asn Met Asn Phe Asp Arg Met Arg Phe
 305 310 315 320

Val Ala Glu Arg Ala Glu Val Gly Glu Ala Arg Glu Ala Val Phe Ala
 325 330 335

Val Thr Ile Pro Glu Glu Arg Gly Ser Phe Lys Arg Phe Cys Ser Leu
 340 345 350

Val Gly Asp Arg Asn Val Thr Glu Phe Asn Tyr Arg Ile Ala Asp Ala
 355 360 365

Gln Ser Ala His Ile Phe Val Gly Val Gln Ile Arg Arg Arg Gly Glu
 370 375 380

Ser Ala Asp Ile Ala Ala Asn Phe Glu Ser His Gly Phe Lys Thr Ala
 385 390 395 400

Asp Leu Thr His Asp Glu Leu Ser Lys Glu His Ile Arg Tyr Met Val
 405 410 415

Gly Gly Arg Ser Pro Leu Ala Leu Asp Glu Arg Leu Phe Arg Phe Glu
 420 425 430

Phe Pro Glu Arg Pro Gly Ala Leu Met Lys Phe Leu Ser Ser Met Ala
 435 440 445

Pro Asp Trp Asn Ile Ser Leu Phe His Tyr Arg Asn Gln Gly Ala Asp
 450 455 460

Tyr Ser Ser Ile Leu Val Gly Leu Gln Val Pro Gln Ala Asp His Ala
 465 470 475 480

Glu Phe Glu Arg Phe Leu Ala Ala Leu Gly Tyr Pro Tyr Val Glu Glu
 485 490 495

Ser Ala Asn Pro Ala Tyr Arg Leu Phe Leu Ser
 500 505

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1582 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: cc3.mn0002d2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACGAGACGAG TCCCCTCCCC CCACCTCGCC TCACCCAACC GGAACGAACA AGTTACCATC	60
TCATCCCAAC CCCGCCTCGA CCGGATCTCG TCGGACTCGG ATCCGCCCGA CCACCCCGCG	120
CCGCCGCAGA TCAAAGAAGA TGGCAGCTCT CGACACCTTC CTCTTCACCT CGGAGTCTGT	180
GAACGAGGGA CACCCTGACA AGCTCTGCGA CCAGGTCTCA GATGCCGTTC TTGACGCTTG	240
CCTTGCTGAG GACCCTGACA GCAAGGTTGC TTGTGAGACC TGCACCAAGA CCAACATGGT	300
CATGGTCTTT GGTGAGATCA CCACCAAGGC CAATGTCGAC TACGAGAAGA TTGTCAGGGA	360
GACCTGCCGC AACATTGGTT TTGTGTCAA CGATGTCGGG CTGACGCTG ACCACTGCAA	420
GGTGCTCGTG AACATTGAGC AGCAGTCCCC TGATATTGCT CAGGGTGTGC ATGGCCACTT	480
CACCAAGCGC CCCGAGGAGA TTGGAGCTGG TGACCAGGGA CACATGTTCT GGTATGCGAC	540

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CGATGAGACC CCTGAGTTGA TGCCCTCAG CCATGTCCTT GCCACCAAGC TAGGTGCTCG      600
TCTCACCGAG GTCCGCAAGA ACGGAACCTG CCCCTGGCTC AGGCCTGATG GGAAGACCCA      660
GGTGACAGTC GAGTACCGCA ATGAGGGTGG TGCCATGGTC CCCATCCGTG TCCACACCGT      720
CCTCATCTCC ACCCAGCACG ACGAGACAGT GACCAATGAT GAGATCGCTG CTGACCTGAA      780
GGAGCATGTC ATCAAGCCTA TCATCCCTGA GCAGTACCTT GACGAGAAGA CCATCTTCCA      840
CCTTAACCCA TCCGGCCGCT TTGTCATTGG TGGACCTCAC GGCATGCTG GCCTCACTGG      900
CCGCAAGATC ATCATTGACA CCTACGGTGG CTGGGGAGCC CATGGCGGTG GCGCTTTCTC      960
CGGCAAGGAC CCAACCAAGG TTGACCGCAG CGGAGCCTAT GTCGCGAGGC AGGCTGCCAA     1020
GAGCATCGTC GCCAGCGGCC TTGCTCGCCG CGCCATCGTC CAGGTGTCCT ACGCCATCGG     1080
CGTGCCCGAG CCTCTCTCCG TGTTTGTGCG CACGTACGGC ACCGGCGCGA TCCCCGACAA     1140
GGAGATCCTC AAGATTGTCA AGGAGAACTT CGATTTTCAGG CCTGGCATGA TTATCATCAA     1200
CCTTGACCTC AAGAAAGGCG GCAACGGGCG CTACCTCAAG ACGGCAGCCT ACGGCCACTT     1260
CGGAAGGGAC GACCCTGACT TCACCTGGGA GGTGGTGAAG CCACTCAAGT CGGAGAAACC     1320
TTCTGCCTAA GCGGCCTTTT TTTTCAGTAA GAAGCTTTTG GTGGTCTGCT GTGCTTAATC     1380
ATGCTTTTAT ATGGCTTCTA CATGTTGTGG TTCTTTCTTG ATCTGCACCG CGCTTATCGT     1440
TTGTGTTGTA CTGCCCTAAT AAGTGGTGCT TATGAGGACT GTTTCTGGTT TTGCTGCTTA     1500
TGTTGTAATG CTTTGAAACA ATGAAAGAAG CTACAGGCCA CAGCTATTTT GAGAAGTAAT     1560
GGAACCTCGT GCCGTTTTGA TT                                             1582

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(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: cc3.mn0002.d2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Met Ala Ala Leu Asp Thr Phe Leu Phe Thr Ser Glu Ser Val Asn Glu
1           5           10           15
Gly His Pro Asp Lys Leu Cys Asp Gln Val Ser Asp Ala Val Leu Asp
20          25          30
Ala Cys Leu Ala Glu Asp Pro Asp Ser Lys Val Ala Cys Glu Thr Cys
35          40          45
Thr Lys Thr Asn Met Val Met Val Phe Gly Glu Ile Thr Thr Lys Ala
50          55          60
Asn Val Asp Tyr Glu Lys Ile Val Arg Glu Thr Cys Arg Asn Ile Gly
65          70          75          80

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Phe Val Ser Asn Asp Val Gly Leu Asp Ala Asp His Cys Lys Val Leu
 85 90 95
 Val Asn Ile Glu Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly
 100 105 110
 His Phe Thr Lys Arg Pro Glu Glu Ile Gly Ala Gly Asp Gln Gly His
 115 120 125
 Met Phe Gly Tyr Ala Thr Asp Glu Thr Pro Glu Leu Met Pro Leu Ser
 130 135 140
 His Val Leu Ala Thr Lys Leu Gly Ala Arg Leu Thr Glu Val Arg Lys
 145 150 155 160
 Asn Gly Thr Cys Pro Trp Leu Arg Pro Asp Gly Lys Thr Gln Val Thr
 165 170 175
 Val Glu Tyr Arg Asn Glu Gly Gly Ala Met Val Pro Ile Arg Val His
 180 185 190
 Thr Val Leu Ile Ser Thr Gln His Asp Glu Thr Val Thr Asn Asp Glu
 195 200 205
 Ile Ala Ala Asp Leu Lys Glu His Val Ile Lys Pro Ile Ile Pro Glu
 210 215 220
 Gln Tyr Leu Asp Glu Lys Thr Ile Phe His Leu Asn Pro Ser Gly Arg
 225 230 235 240
 Phe Val Ile Gly Gly Pro His Gly Asp Ala Gly Leu Thr Gly Arg Lys
 245 250 255
 Ile Ile Ile Asp Thr Tyr Gly Gly Trp Gly Ala His Gly Gly Gly Ala
 260 265 270
 Phe Ser Gly Lys Asp Pro Thr Lys Val Asp Arg Ser Gly Ala Tyr Val
 275 280 285
 Ala Arg Gln Ala Ala Lys Ser Ile Val Ala Ser Gly Leu Ala Arg Arg
 290 295 300
 Ala Ile Val Gln Val Ser Tyr Ala Ile Gly Val Pro Glu Pro Leu Ser
 305 310 315 320
 Val Phe Val Asp Thr Tyr Gly Thr Gly Ala Ile Pro Asp Lys Glu Ile
 325 330 335
 Leu Lys Ile Val Lys Glu Asn Phe Asp Phe Arg Pro Gly Met Ile Ile
 340 345 350
 Ile Asn Leu Asp Leu Lys Lys Gly Gly Asn Gly Arg Tyr Leu Lys Thr
 355 360 365
 Ala Ala Tyr Gly His Phe Gly Arg Asp Asp Pro Asp Phe Thr Trp Glu
 370 375 380
 Val Val Lys Pro Leu Lys Ser Glu Lys Pro Ser Ala
 385 390 395

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2183 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Oryza sativa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCTTAT AAATGAACGG AAAATGGAAA AAAAAATTGA TTGGTGCCAC TTCAAAGTTA	60
AATATGCCAA GACGAATTGA TATGTTTCTG CTGTTGTTTT ATGCTCTTGA TTAGTTGATG	120
CGCATGTTCA ATGATTTATG ATGTTTGTCT TTGTGGAAAG ATTACATGTA AAGAGTATAG	180
TAGAACCCTT AAAAGCTAGC CAGCGATTTC GCTCTTTTTT TCCAGGTCTC CATGATATGT	240
TTACCCCTAA AAGTGGTATA TTTATGTGAT AGTTACAATA CATAGTGGAC CACGATTGAT	300
TATGCGTTTA TGCTGATTCC GGCAGAAAAT TGTTAGATTC CTTGTGCTCT ATACCTGCTT	360
GTTGCGCTTG TAGAGAATAT TACAAATACC TAACACTTGC CCAAGGAACT TAGGAACTTA	420
GTCAACTCTT TGTAGGGACA ACTATTTTAG CCCAAAATTG TGGTCTTGTC AGGTGCCAAC	480
AAAACAGCAT CTTGGCGTAC ATAAGCTATA TAGAGGATTA AAAGGAATGT TTTGTTCCCT	540
GCTACTGTTT TTTTAACCTG TTTACTCAGG ACAAATTTTG TTGCATAAAC CATTTGTCTT	600
AGGGATCAGT ATTGTCCTCT CAGTGTGTTA TGTAAGCATT TCCAGAAATC AATTGTCGCT	660
ATCAGCTTCC CTCACATTAG CTATCACTTA TACCCCTTTT TTTCTCATAG GCTCACCATG	720
TCCATTTTAT TCATGATATT TCTTGTCTA AAGTATGTGA AATACCATTT TATGCAGATA	780
GGAGAAGATG GCCGCACTTG ATACCTTCCT CTTTACCTCG GAGTCTGTGA ACGAGGGCCA	840
CCCTGACAAG CTCTGCGACC AAGTCTCAGA TGCTGTGCTT GATGCCTGCC TCGCCGAGGA	900
CCCTGACAGC AAGGTCGCTT GTGAGACCTG CACCAAGACA AACATGGTCA TGGTCTTTGG	960
TGAGATCACC ACCAAGGCTA ACGTTGACTA TGAGAAGATT GTCAGGGAGA CATGCCGTAA	1020
CATCGGTTTT GTGTCAGCTG ATGTCGGTCT CGATGCTGAC CACTGCAAGG TGCTTGTGAA	1080
CATCGAGCAG CAGTCCCCTG ACATTGCACA GGGTGTGCAC GGGCACTTCA CCAAGCGCCC	1140
TGAGGAGATT GGTGCTGGTG ACCAGGGACA CATGTTTGA TATGCAACTG ATGAGACCCC	1200
TGAGTTGATG CCCCTCAGCC ATGTCCTTGC TACCAAGCTT GGCCTCGTC TTACGGAGGT	1260
TCGCAAGAAT GGGACCTGCG CATGGCTCAG GCCTGACGGG AAGACCCAAG TGAAGTTGA	1320
GTACCGCAAT GAGAGCGGTG CCAGGGTCCC TGTCCTGTG CACACCGTCC TCATCTCTAC	1380
CCAGCATGAT GAGACAGTCA CCAACGATGA GATTGCTGCT GACCTGAAGG AGCATGTCAT	1440
CAAGCCTGTC ATTCCCGAGC AGTACCTTGA TGAGAAGACA ATCTTCCATC TTAACCCATC	1500
TGGTCGCTTC GTCATTGGCG GACCTCATGG TGATGCTGGT CTCACTGGCC GGAAGATCAT	1560
CATTGACACT TATGGTGGCT GGGGAGCTCA CGGTGGTGGT GCCTTCTCTG GCAAGGACCC	1620
AACCAAGGTT GACCGCAGTG GAGCATACGT CGCAAGGCAA GCTGCCAAGA GCATTGTTGC	1680

TAGTGGCCTT GCTCGCCGCT GCATTGTCCA AGTATCATAC GCCATCGGTG TCCCAGAGCC	1740
ACTGTCCGTA TTCGTGACATA CACACGGCAC TGGCAGGATC CCTGACAAGG AGATCCTCAA	1800
GATTGTGAAG GAGAACTTCG ACTTCAGGCC TGGCATGATC ATCATCAACC TTGACCTCAA	1860
GAAAGGCGGC AACGGACGCT ACCTCAAGAC GCGGGCTTAC GGTCACCTCG GAAGGGACGA	1920
CCCAGACTTC ACCTGGGAGG TGGTGAAGCC CCTCAAGTGG GAGAAGCCTT CTGCCTAAAA	1980
GCTCCCTTTC GGAGGCTTTT GCTCTGTCCC ATTATGGTGT TTTGTTTCCT CGCTGCTCAG	2040
CATTGTGATT CTTAACCTGC CCCCCGCTGC CATTTATGCC CATGCACGCT ACTTTCCTAA	2100
TAATAAGTAC TTATAAGGGT ATTGTGTTTG AATATTTTAC CTAGAGGAGG AGGAGGATTT	2160
GTTATCTGTT ATTGCTTAAG CTT	2183

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: s2.12b06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGCCAAGCCC CACTCAACCA CCACACCACT CTCTCTGCTC TTCTTCTACC TTTCAAGTTT	60
TTAAAGTATT AAGATGGCAG AGACATTCTT ATTTACCTCA GAGTCAGTGA ACGAGGGACA	120
CCCTGACAAG CTCTGCGACC AAATCTCCGA TGCTGTCTC GACGCTTGCC TTGAACAGGA	180
CCCAGACAGC AAGGTTGCCT GCGAAACATG CACCAAGACC AACTTGGTCA TGGTCTTCGG	240
AGAGATCACC ACCAAGGCCA ACGTTGACTA CGAGAAGATC GTGCGTGACA CCTGCAGGAA	300
CATCGGCTTC GTCTCAAACG ATGTGGGACT TGATGCTGAC AACTGCAAGG TCCTTGTA	360
CATTGAGCAG CAGAGCCCTG ATATTGCCCA GGGTGTGCAC GGCCACCTTA CCAAAGACC	420
CGAGGAAATC GGTGCTGGAG ACCAGGGTCA CATGTTTGGC TATGCCACGG ACGAAACCCC	480
AGAATTGATG CCATTGAGTC ATGTTCTTGC AACTAAACTC GGTGCTCGTC TCACCGAGGT	540
TCGCAAGAAC GGAACCTGCC CATGGTTGAG GCCTGATGGG AAAACCCAAG TGA	600
GTATTACAAT GACAACGGTG CCATGGTTCC AGTTCGTGTC CACTGTGTC TTATCTCCAC	660
CCAACATGAT GAGACTGTGA CCAACGACGA AATTGCAGCT GACCTCAAGG AGCATGTGAT	720
CAAGCCGGTG ATCCCGGAGA AGTACCTTGA TGAGAAGACC ATTTTCCACT TGAACCCCTC	780
TGGCCGTTTT GTCATTGGAG GTCCTCACGG TGATGCTGGT CTCACCGGCC GCAAGATCAT	840
CATCGATACT TACGGAGGAT GGGGTGCTCA TGGTGGTGGT GCTTCTCCG GGAAGGATCC	900
CACCAAGGTT GATAGGAGTG GTGCTTACAT TGTGAGACAG GCTGCTAAGA GCATTGTGGC	960
AAGTGGAATA GCCAGAAGGT GCATTGTGCA AGTGTCTTAT GCCATTGGTG TGCCCGAGCC	1020

TTTGTCTGTC TTTGTTGACA CCTATGGCAC CGGGAAGATC CATGATAAGG AGATTCTCAA 1080
 CATTGTGAAG GAGAACTTTG ATTTTCAGGCC CGGTATGATC TCCATCAACC TTGATCTCAA 1140
 GAGGGGTGGG AATAACAGGT TCTTGAAGAC TGCTGCATAT GGACACTTCG GCAGAGAGGA 1200
 CCCTGACTTC ACATGGGAAG TGGTCAAGCC CCTCAAGTGG GAGAAGGCCT AAGGCCATTC 1260
 ATTCCACTGC AATGTGCTGG GAGTTTTTTA GCGTTGCCCT TATAATGTCT ATTATCCATA 1320
 ACTTTCCACG TCCCTTGCTC TGTGTTTTTC TCTCGTCGTC CTCCTCCTAT TTTGTTTCTC 1380
 CTGCCTTTCA TTTGTAATTT TTTACATGAT CAACTAAAAA ATGTACTCTC TGTTTTCCGA 1440
 CCATTGTGTC TCTTAATATC AGTATCAAAA AGAATGTTCC AAGTT 1485

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: s2.12b06

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Ala Glu Thr Phe Leu Phe Thr Ser Glu Ser Val Asn Glu Gly His
 1 5 10 15
 Pro Asp Lys Leu Cys Asp Gln Ile Ser Asp Ala Val Leu Asp Ala Cys
 20 25 30
 Leu Glu Gln Asp Pro Asp Ser Lys Val Ala Cys Glu Thr Cys Thr Lys
 35 40 45
 Thr Asn Leu Val Met Val Phe Gly Glu Ile Thr Thr Lys Ala Asn Val
 50 55 60
 Asp Tyr Glu Lys Ile Val Arg Asp Thr Cys Arg Asn Ile Gly Phe Val
 65 70 75 80
 Ser Asn Asp Val Gly Leu Asp Ala Asp Asn Cys Lys Val Leu Val Asn
 85 90 95
 Ile Glu Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly His Leu
 100 105 110
 Thr Lys Arg Pro Glu Glu Ile Gly Ala Gly Asp Gln Gly His Met Phe
 115 120 125
 Gly Tyr Ala Thr Asp Glu Thr Pro Glu Leu Met Pro Leu Ser His Val
 130 135 140
 Leu Ala Thr Lys Leu Gly Ala Arg Leu Thr Glu Val Arg Lys Asn Gly
 145 150 155 160
 Thr Cys Pro Trp Leu Arg Pro Asp Gly Lys Thr Gln Val Thr Val Glu
 165 170 175

Tyr Tyr Asn Asp Asn Gly Ala Met Val Pro Val Arg Val His Thr Val
 180 185 190
 Leu Ile Ser Thr Gln His Asp Glu Thr Val Thr Asn Asp Glu Ile Ala
 195 200 205
 Ala Asp Leu Lys Glu His Val Ile Lys Pro Val Ile Pro Glu Lys Tyr
 210 215 220
 Leu Asp Glu Lys Thr Ile Phe His Leu Asn Pro Ser Gly Arg Phe Val
 225 230 235 240
 Ile Gly Gly Pro His Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile
 245 250 255
 Ile Asp Thr Tyr Gly Gly Trp Gly Ala His Gly Gly Gly Ala Phe Ser
 260 265 270
 Gly Lys Asp Pro Thr Lys Val Asp Arg Ser Gly Ala Tyr Ile Val Arg
 275 280 285
 Gln Ala Ala Lys Ser Ile Val Ala Ser Gly Leu Ala Arg Arg Cys Ile
 290 295 300
 Val Gln Val Ser Tyr Ala Ile Gly Val Pro Glu Pro Leu Ser Val Phe
 305 310 315 320
 Val Asp Thr Tyr Gly Thr Gly Lys Ile His Asp Lys Glu Ile Leu Asn
 325 330 335
 Ile Val Lys Glu Asn Phe Asp Phe Arg Pro Gly Met Ile Ser Ile Asn
 340 345 350
 Leu Asp Leu Lys Arg Gly Gly Asn Asn Arg Phe Leu Lys Thr Ala Ala
 355 360 365
 Tyr Gly His Phe Gly Arg Glu Asp Pro Asp Phe Thr Trp Glu Val Val
 370 375 380
 Lys Pro Leu Lys Trp Glu Lys Ala
 385 390

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Lycopersicon esculentum*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAATTCCTAC AAAGAGGTTA TTTCTCTCAA GGGGTAAAAA GATTGCCCTT TTTGACATT	60
TATAATCCTC TTTTCTCTT TGTCGCCGT TGGGTCTTC ACTTTCCTGT TTCTTGAGAA	120
TGGAACTTT CTTATTCACC TCCGAGTCTG TGAACGAGGG TCACCCAGAG AAGCTCTGTG	180
ATCAGATCTC TGATGCAGTT CTTGATGCCT GCCTTGAGCA AGATCCCGAG AGCAAAGTTG	240
CATGTGAAAC TTGCACCAAG ACCAACTTGG TCATGGTCTT TGGTGAGATC ACAACCAAGG	300

CTATTGTAGA CTATGAGAAG ATTGTGCGTG ACACATGCCG TAATATTGGA TTTGTTTCTG	360
ATGATGTTGG TCTTGATGCT GACAACTGCA AGGTCCTTGT TTACATTGAG CAGCAAAGTC	420
CTGATATTGC TCAAGGTGTC CACGGCCATC TGACCAAACG CCCCAGGAG ATTGGTGCTG	480
GTGACCAGGG CCACATGTTT GGCTATGCAA CAGATGAGAC CCCTGAATTA ATGCCTCTCA	540
GTCACGTGCT TGCAACTAAA CTTGGTGCCC GTCTTACAGA AGTCCGCAAG AATGGCACCT	600
GCGCCTGGTT GAGGCCTGAT GGCAAGACCC AAGTTACTGT TGAGTATAGC AATGACAATG	660
GTGCCATGGT TCCAATTAGG GTACACACTG TTCTTATCTC CACCCAACAC GATGAGACCG	720
TTACCAATGA TGAGATTGCC CGCGACCTTA AGGAGCATGT CATCAAACCA GTCATCCCAG	780
AGAAGTACCT TGATGAGAAT ACTATTTTCC ACCTTAACCC ATCTGGCCGA TTCGTTATTG	840
GTGGACCTCA TGGTGATGCT GGTCTCACTG GTCGTAAAAT CATCATCGAC ACTTATGGTG	900
GTGGGGTGC TCATGGTGGT GGTGCTTTCT CGGGCAAAGA CCAACCAAG GTCGACAGGA	960
GTGGTGCATA CATTGTAAGG CAGGCTGCAA AGAGTATCGT AGCTAGTGGA CTTGCTCGTA	1020
GATGCATCGT GCAGGTATCT TATGCCATCG GTGTGCCTGA GCCATTGTCT GTATTCGTTG	1080
ACACCTATGG CACTGGAAAG ATCCCTGACA GGGAAATTTT GAAGATCGTT AAGGAGAACT	1140
TTGACTTCAG ACCTGGAATG ATGTCCATTA ACTTGATTTT GAAGAGGGGT GGCAATAGAA	1200
GATTCTTGAA AACTGCTGCC TATGGTCACT TTGGACGTGA TGACCCCGAT TTCACATGGG	1260
AAGTTGTCAA GCCCCTCAAG TGGGAAAAGC CCAAGACTA ATAAGTGCTT GCCTATGTTT	1320
TTGTTCTTTG TTGTTTGCTT GTGGCTTTAG AATCTCCCC GTGTTTGCTT GTTTGTCTTT	1380
GTATTTTCTC TTTTGACCCT TTATTTTGTT ATTGTCCTGT TTCCATTGTG TTGGATGGAT	1440
ATCTTAGGCC TTGGAATATT AAGGAAAGAA AAGGAATTC	1479

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCTCCCTTC GGTTCAATCGG CCTCCCGATC GAGCAGTAGA AGCAGCGCAA GGGCATCGCT	60
AGCACTAAAG AAATGGCAGC CGAGACGTTT CTCTTCACGT CCGAGTCTGT GAACGAGGGC	120
CATCCCGACA AGCTCTGTGA CCAAGTCTCC GACGCCGTCT TGGATGCCTG CTTGGCCCCAG	180
GATGCCGACA GCAAGGTGCG CTGCGAGACC GTCACCAAGA CCAACATGGT CATGGTCTTG	240
GGCGAGATCA CCACCAAGGC CACCGTCGAC TATGAGAAGA TCGTGCGTGA CACCTGCCGC	300
AACATCGGTT TCATCTCTGA TGACGTTGGT CTCGACGCCG ACCGTTGCAA RGTGCTCGTC	360
AACATCGAGC AGCAGTCCCC TGACATTGCC CAGGGTGTTT ATGGACACTT CACCAAGCGT	420

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CCCGAAGAAG TCGGCGCCGG TGACCAGGGC ATCATGTTCTG GCTATGCCAC CGATGAGACC      480
CCTGAGCTGA TGCCCCCTCA GCACGTGCTT GCCACCAAGC TYGGAGCTCG CCTCACSGAG      540
GTCCGCAAGA ATGGCACCTG CGCCTGGGTC AGGCCTGACG GAAAGACCCA GGTACACAGTC      600
GAGTACCTAA ACGAGGATGG TGCCATGGTA CTTGTTCTGTG TGCACACCGT CCTCATCTCC      660
ACCCAGCACG ACGAGACCGT CACCAACGAC GAGATTGCTG CGGACCTCAA GGAGCATGTC      720
ATCAAGCCGG TGATCCCCGC AAAGTACCTC GATGAGAACA CCATCTTCCA CCTGAACCCG      780
TCTGGCCGCT TCGTCATCGG CGGCCCCCAC GGTGACGCCG GTCTCACCGG CCGCAAGATC      840
ATCATCGACA CCTATGGTGG CTGGGGAGCC CACGGCGGCG GTGCCTTCTC TGGCAAGGAC      900
CCAACCAAGG TCGACCGYAG TGGCGCCTAC ATTGCCAGGC ARGCCGCCAA GAGCATCATC      960
GCCAGCGGCC TCGCACGCCG CTGCATTGTG CAGATCTCAT ACGCCATCGG TGTGCCTGAG     1020
CCTTTGTCTG TGTTCTGTCG CTCCTACGGC ACCGGCAAGA TCCCCGACAG GGAGATCCTC     1080
AAGCTCGTGA AGGAGAACTT TGACTTCAGG CCCGGGATGA TCAGCATCAA CCTGGACTTG     1140
AAGAAAGGTG GAAACAGGTT CATCAAGACC GCTGCTTACG GTCACCTTGG CCGTGATGAT     1200
GCCGACTTCA CCTGGGAGGT GGTGAAGCCC CTCAAGTTCG ACAAGGCATC TGCCTAAGAG     1260
CATGGCATTG TCTTGCTCTG CCGCCTCTCA AGTTCGTCAA GACGGGATCA TGTTGCTCCT     1320
GGGAAGTGGG AAGAAGCATT AGACATTGAA GCGACGCTCT ACACTGGTCT TGTTGTATGG     1380

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(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 394 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

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Met Ala Ala Glu Thr Phe Leu Phe Thr Ser Glu Ser Val Asn Glu Gly
1           5           10          15
His Pro Asp Lys Leu Cys Asp Gln Val Ser Asp Ala Val Leu Asp Ala
20          25          30
Cys Leu Ala Gln Asp Ala Asp Ser Lys Val Ala Cys Glu Thr Val Thr
35          40          45
Lys Thr Asn Met Val Met Val Leu Gly Glu Ile Thr Thr Lys Ala Thr
50          55          60
Val Asp Tyr Glu Lys Ile Val Arg Asp Thr Cys Arg Asn Ile Gly Phe
65          70          75          80
Ile Ser Asp Asp Val Gly Leu Asp Ala Asp Arg Cys Lys Val Leu Val
85          90          95
Asn Ile Glu Gln Gln Ser Pro Asp Ile Ala Gln Gly Val His Gly His
100         105         110

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Phe Thr Lys Arg Pro Glu Glu Val Gly Ala Gly Asp Gln Gly Ile Met
 115 120 125
 Phe Gly Tyr Ala Thr Asp Glu Thr Pro Glu Leu Met Pro Leu Lys His
 130 135 140
 Val Leu Ala Thr Lys Leu Gly Ala Arg Leu Thr Glu Val Arg Lys Asn
 145 150 155 160
 Gly Thr Cys Ala Trp Val Arg Pro Asp Gly Lys Thr Gln Val Thr Val
 165 170 175
 Glu Tyr Leu Asn Glu Asp Gly Ala Met Val Pro Val Arg Val His Thr
 180 185 190
 Val Leu Ile Ser Thr Gln His Asp Glu Thr Val Thr Asn Asp Glu Ile
 195 200 205
 Ala Ala Asp Leu Lys Glu His Val Ile Lys Pro Val Ile Pro Ala Lys
 210 215 220
 Tyr Leu Asp Glu Asn Thr Ile Phe His Leu Asn Pro Ser Gly Arg Phe
 225 230 235 240
 Val Ile Gly Gly Pro His Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile
 245 250 255
 Ile Ile Asp Thr Tyr Gly Gly Trp Gly Ala His Gly Gly Gly Ala Phe
 260 265 270
 Ser Gly Lys Asp Pro Thr Lys Val Asp Arg Ser Gly Ala Tyr Ile Ala
 275 280 285
 Arg Gln Ala Ala Lys Ser Ile Ile Ala Ser Gly Leu Ala Arg Arg Cys
 290 295 300
 Ile Val Gln Ile Ser Tyr Ala Ile Gly Val Pro Glu Pro Leu Ser Val
 305 310 315 320
 Phe Val Asp Ser Tyr Gly Thr Gly Lys Ile Pro Asp Arg Glu Ile Leu
 325 330 335
 Lys Leu Val Lys Glu Asn Phe Asp Phe Arg Pro Gly Met Ile Ser Ile
 340 345 350
 Asn Leu Asp Leu Lys Lys Gly Gly Asn Arg Phe Ile Lys Thr Ala Ala
 355 360 365
 Tyr Gly His Phe Gly Arg Asp Asp Ala Asp Phe Thr Trp Glu Val Val
 370 375 380
 Lys Pro Leu Lys Phe Asp Lys Ala Ser Ala
 385 390

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hordeum vulgare*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAATTCGGGA TAGCATCAGC ACAACTGCAC GAGAGCATCT CTACCACCAA AGAAATGGCG	60
GCCGAGACGT TCCTCTTCAC GTCCGAGTCC GTGAACGAGG GCCATCCCGA CAAGCTGTGC	120
GACCAGGTCT CTGACGCCGT CTTGGACGCC TGCTTGCCCC AGGATCCTGA CAGCAAGGTT	180
GCTTGCGAGA CCTGCACCAA GACCAACATG GTCATGGTCT TCGGCGAGAT CACCACCAAG	240
GCCACCGTTG ACTATGAGAA GATTGTGCGC GACACCTGCC GTGACATCGG CTTTCATCTCT	300
GACGACGTCG GTCTCGATGC CGACCATTGC AAGGTGCTCG TCAACATCGA GCAGCAATCC	360
CCTGACATTG CCCAGGGTGT TCACGGACAC TTCACCAAGC GTCCAGAAGA GGTCGGCGCC	420
GGTGACCAGG GCATCATGTT TGGCTACGCC ACTGATGAGA CCCCTGAGCT GATGCCCCCTC	480
ACCCACATGC TTGCCACCAA GCTCGGAGCT CGCCTCACCG AGGTCCGCAA GAATGGCACC	540
TGCGCCTGGC TCAGGCCTGA TGGAAAGACC CAGGTCACCA TTGAGTACCT AAACGAGGGT	600
GGTGCCATGG TGCCCGTTCG TGTGCACACC GTCCTCATCT CCACCCAGCA TGATGAGACC	660
GTCACCAACG ATGAGATCGC TGCAGACCTC AAGGAGCATG TCATCAAGCC GGTGATTCCC	720
GGGAAGTACC TCGATGAGAA CACCATCTTC CACCTGAACC CATCGGGCCG CTTTGTTCATC	780
GGTGCCCTC ACGGCGATGC CGGTCTCACC GCCCGCAAGA TCATCATCGA CACCTATGGT	840
GGCTGGGGAG CCCACGGCGG CGGTGCCTTC TCTGGCAAGG ACCCTACCAA GGTCGACCGC	900
AGTGGCGCCT ACATTGCCAG GCAGGCTGCC AAGAGCATCA TCGCCAGCGG CCTCGCACGC	960
CGGTGCATTG TGCAGATCTC ATATGCCATC GGTGTACCTG AGCCTTTGTC TGTGTTTCGTC	1020
GACTCCTACG GCACTGGCAA GATCCCTGAC AGGGAGATCC TCAAGCTCGT GAAGGAGAAC	1080
TTTGAATTCA GACCCGGGAT GATCACGATC AACCTCGACT TGAAGAAAGG TGGAAACAGG	1140
TTCATCAAGA CAGCTGCTTA CGGTCACTTT GGCCGCGATG ATGCTGACTT CACCTGGGAG	1200
GTGGTGAAGC CCCTCAAGTT CGACAAGGCA TCTGCTTAAG AAGAAGACAT CACATTGAGG	1260
GTTCTTCTTG GTCTGATGCC TCTCAAGTTC GGCAAGGCGG GATCCTTTTG CTCCTCGGAA	1320
GTAAGAAGAA GCATTCAACA TCGCCCGGAA TTC	1353